



SEQUENCE LISTING

<110> Lechler, Robert  
Dorling, Anthony

<120> IMMUNOSUPPRESSION BY BLOCKING T CELL CO-STIMULATION

<130> 02292/000H795-US0

<140> US 09/674,462

<141> 2001-05-08

<150> PCT/GB99/01350

<151> 1999-04-30

<150> GB-9809280.2

<151> 1998-04-30

<160> 35

<170> PatentIn Ver. 2.1

<210> 1

<211> 223

<212> PRT

<213> Sus scrofa

<400> 1

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Val Phe Ser Lys Gly Met His Val Ala Gln Pro Ala Val Val Leu Ala  
35 40 45  
Asn Ser Arg Gly Val Ala Ser Phe Val Cys Glu Tyr Gly Ser Ala Gly  
50 55 60  
Lys Ala Ala Glu Val Arg Val Thr Val Leu Arg Arg Ala Gly Ser Gln  
65 70 75 80  
Met Thr Glu Val Cys Ala Ala Thr Tyr Thr Val Glu Asp Glu Leu Thr  
85 90 95  
Phe Leu Asp Asp Ser Thr Cys Thr Gly Thr Ser Thr Glu Asn Lys Val  
100 105 110  
Asn Leu Thr Ile Gln Gly Leu Arg Ala Val Asp Thr Gly Leu Tyr Ile  
115 120 125  
Cys Lys Val Glu Leu Leu Tyr Pro Pro Pro Tyr Tyr Val Gly Met Gly  
130 135 140  
Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser  
145 150 155 160  
Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe  
165 170 175  
Tyr Ser Phe Leu Ile Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys  
180 185 190

Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu  
195 200 205  
Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn  
210 215 220

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<213> Sus scrofa

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gccaacctg cagtagtgct ggccaacagc cggggtgttg ccagctttgt gtgtgagtat 180  
gggtctgcag gcaaagctgc cgaggtccgg gtgacagtgc tgcggcgggc cggcagccag 240  
atgactgaag tctgtgccgc gacatatact gtggaggatg agttgacctt ccttgatgac 300  
tctacatgca ctggcacctc caccgaaaac aaagtgaacc tcaccatcca agggctgaga 360  
gccgtggaca ctgggctcta catctgcaag gtggagctcc tgtaccacc accctactat 420  
gtgggtatgg gcaacgggac ccagatttat gtcattgatc cagaaccatg cccagattct 480  
gatttcctgc tctggatcct ggcagcagtt agttcagggt tgttttttta cagcttcctc 540  
atcacagctg tttctttgag caaaatgcta aagaaaagaa gtcctcttac tacaggggtc 600  
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cccatcaatt ga 672

<210> 3  
<211> 400  
<212> PRT  
<213> Artificial Sequence

<220>  
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20 25 30  
Val Phe Ser Lys Gly Met His Val Ala Gln Pro Ala Val Val Leu Ala  
35 40 45  
Asn Ser Arg Gly Val Ala Ser Phe Val Cys Glu Tyr Gly Ser Ala Gly  
50 55 60  
Lys Ala Ala Glu Val Arg Val Thr Val Leu Arg Arg Ala Gly Ser Gln  
65 70 75 80  
Met Thr Glu Val Cys Ala Ala Thr Tyr Thr Val Glu Asp Glu Leu Thr  
85 90 95  
Phe Leu Asp Asp Ser Thr Cys Thr Gly Thr Ser Thr Glu Asn Lys Val  
100 105 110  
Asn Leu Thr Ile Gln Gly Leu Arg Ala Val Asp Thr Gly Leu Tyr Ile  
115 120 125  
Cys Lys Val Glu Leu Leu Tyr Pro Pro Pro Tyr Tyr Val Gly Met Gly  
130 135 140  
Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser

145                      150                      155                      160  
 Asp Gly Gly Ser Gly Gly Ala Ala Glu Pro Lys Ser Cys Asp Lys Thr  
                                  165                      170                      175  
 His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser  
                                  180                      185                      190  
 Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg  
                                  195                      200                      205  
 Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro  
                                  210                      215                      220  
 Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala  
                                  225                      230                      235                      240  
 Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val  
                                  245                      250                      255  
 Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr  
                                  260                      265                      270  
 Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr  
                                  275                      280                      285  
 Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu  
                                  290                      295                      300  
 Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys  
                                  305                      310                      315                      320  
 Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser  
                                  325                      330                      335  
 Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp  
                                  340                      345                      350  
 Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser  
                                  355                      360                      365  
 Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala  
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<210> 4  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Phage library

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 ctccagggaa ggggctggag tgggtctcag ctattcgtgg tagtgggtgg agcacatact 180  
 acgcagactc cgtgaagggc cggttcacca tctccagaga caattccaag aacacgctgt 240  
 atctgcaaat gaacagcctg agagccgagg acacggccgt gtattactgt gcaagagctg 300  
 gtcgtatttt gtttgactat tggggccaag gtaccctggg caccgtctcg agtgggtggag 360  
 gcggttcagg cggaggtggc tctggcggtg gtgcacttca gtctgtgctg actcagccac 420

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cctcagcgtc tgggaccccc gggcagcggg tcaccatctc ttgttctgga agcagctcca 480
acatcggaag taattatgta tactgggtacc agcagctccc aggaacggcc cccaaactcc 540
tcatttatag gaataatcag cggccctcag gggtccttga ccgattctct ggctccaagt 600
ctggcacctc agcctccctg gccatcagtg ggctccggtc cgaggatgag gctgattatt 660
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<210> 5  
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 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Phage library

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 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Arg Ala Gly Arg Ile Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu  
 100 105 110  
 Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly  
 115 120 125  
 Gly Ser Ala Leu Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly  
 130 135 140  
 Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn  
 145 150 155 160  
 Ile Gly Ser Asn Tyr Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala  
 165 170 175  
 Pro Lys Leu Leu Ile Tyr Arg Asn Asn Gln Arg Pro Ser Gly Val Pro  
 180 185 190  
 Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile  
 195 200 205  
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 210 215 220  
 Asp Asp Ser Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
 225 230 235 240

<210> 6

<211> 729  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Phage Library

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 ccaggctcca ggggaagggc tggagtgggt ctgagctatt agtggtagtg gtggtagcac 180  
 atactacgca gactccgtga agggccggtt caccatctcc agagacaatt ccaagaacac 240  
 gctgtatctg caaatgaaca gcctgagagc cgaggacacg gccgtgtatt actgtgcaag 300  
 agctggctcg attttgtttg actattgggg ccaaggtacc ctggtcaccg tctcgagtgg 360  
 tggaggcggt tcaggcggag gtggctctgg cggtagtga cttcagtctg tgctgactca 420  
 gccaccctca gcgtctggga cccccgggca gagggtcacc atctcttggt ctggaagcag 480  
 ctccaacatc ggaagtaatt atgtatactg gtaccagcag ctcccaggaa cggcccccaa 540  
 actcctcatc tataggaata atcagcggcc ctgaggggtc cctgaccgat tctctggctc 600  
 caagtctggc acctcagcct ccctggccat cagtgggctc cgggccgagg atgaggctga 660  
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<210> 7  
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 <212> DNA  
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 ccggcagccc ccagggaagg gactggagtg gattgggtat atctattaca gtgggagcac 180  
 caactacaac cctccctca agagtcgagt caccatatca gtagacacgt ccaagaacca 240  
 gttctccctg aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgcaag 300  
 aatgcggaag gataagtttg actattgggg ccaaggtacc ctggtcaccg tctcgagtgg 360  
 tggaggcggt tcaggcggag gtggctctgg cggtagtga cttcagtctg tgctgactca 420  
 gccaccctca gcgtctggga cccccgggca gagggtcacc atctcttggt ctggaagcag 480  
 ctccaacatc ggaagtaatt atgtatactg gtaccagcag ctcccaggaa cggcccccaa 540  
 actcctcatc tataggaata atcagcggcc ctgaggggtc cctgaccgat tctctggctc 600  
 caagtctggc acctcagcct ccctggccat cagtgggctc cgggccgagg atgaggctga 660  
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 cgtccctaggt gcggccgc 738

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 <211> 739  
 <212> DNA  
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<220>  
 <223> Phage Library

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 caggccccctg gacaagggct tgagtggatg ggaataatca accctagtgg tggtagcaca 180  
 caagctacgc acagaagttc cagggcagag tcaccatgac cagggacacg tccacgagca 240  
 cagtctacat ggagctgagc agcctgagat ctgaggacac ggccgtgtat tactgtgcaa 300  
 gaatggctcc ctatgtgaat acgcttgttt tttggggcca aggtaccctg gtcaccgtct 360  
 cgagtgggtg aggcgggtca ggcgagggtg gctctggcgg tagtgactt cagtctgtgc 420  
 tgactcagga ccctgctgtg tctgtggcct tgggacagac agtcaggatc acatgccaa 480

taggagacag	cctcagaagc	tattatgcaa	gctggtacca	gcagaagcca	ggacaggccc	540
ctgtacttgt	catctatggg	aaaaacaacc	ggccctcagg	gatcccagac	cgattctctg	600
gctccagctc	aggaaacaca	gcttccttga	ccatcactgg	ggctcaggcg	gaagatgagg	660
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agctgaccgt	cctaggtgc					739

<210> 9  
 <211> 729  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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gccagatgcc	cgggaaaggc	ctggagtgga	tggggatcat	ctatcctggg	gactctgata	180
ccagatacag	cccgtccttc	caaggccagg	tcaccatctc	agccgacaag	tccatcagca	240
ccgcctacct	gcagtggagc	agcctgaagg	cctcggacac	ggccgtgtat	tactgtgcaa	300
gattttcgcg	tggtggtttt	gactattggg	gccaaggtag	cctggtcacc	gtctcgagtg	360
gtggaggcgg	ttcaggcgga	ggtggctctg	gcggtagtgc	acttgacatc	cagttgaccc	420
agtctccatg	ttcctgtctg	catctgtagg	agacagagtc	accatcactt	gccgggccag	480
tcagggcatt	agcagttatt	tagcctggta	tcagcaaaaa	ccagggaag	cccctaagct	540
cctgggtctat	gctgcatcca	ctttgcaaag	tgggggccca	tcaagggtca	gcggcagtg	600
atctgggaca	gaattcactc	tcacaatcag	cagcctgcag	cctgaagatt	ttgcaactta	660
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caaacgtgc						729

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 <211> 240  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Phage library

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Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Tyr
			20					25					30	
Ala	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp
	35						40					45		
Ser	Ala	Ile	Ser	Gly	Ser	Gly	Gly	Ser	Thr	Tyr	Tyr	Ala	Asp	Ser
	50					55					60			
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu
65					70					75				80
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Cys
				85					90				95	
Ala	Arg	Ala	Gly	Arg	Ile	Leu	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr
			100					105					110	
Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser
			115				120					125		

Gly Ser Ala Leu Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly  
 130 135 140  
 Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn  
 145 150 155 160  
 Ile Gly Ser Asn Tyr Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala  
 165 170 175  
 Pro Lys Leu Leu Ile Tyr Arg Asn Asn Gln Arg Pro Ser Gly Val Pro  
 180 185 190  
 Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile  
 195 200 205  
 Ser Gly Leu Arg Ser Glu Asp Glu Ala Ser Tyr Tyr Cys Ala Ala Trp  
 210 215 220  
 Asp Asp Ser Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
 225 230 235 240

<210> 11  
 <211> 246  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Phage library

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 20 25 30  
 Ser Gly Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly  
 35 40 45  
 Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn  
 50 55 60  
 Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn  
 65 70 75 80  
 Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
 85 90 95  
 Tyr Tyr Cys Ala Arg Met Arg Lys Asp Lys Phe Asp Tyr Trp Gly Gln  
 100 105 110  
 Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly  
 115 120 125  
 Gly Ser Gly Gly Ser Ala Leu Gln Ser Val Leu Thr Gln Pro Pro Ser  
 130 135 140  
 Ala Ser Gly Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser  
 145 150 155 160  
 Ser Ser Asn Ile Gly Ser Asn Tyr Val Tyr Trp Tyr Gln Gln Leu Pro  
 165 170 175

Gly Thr Ala Pro Lys Leu Leu Ile Tyr Arg Asn Asn Gln Arg Pro Ser  
 180 185 190  
 Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser  
 195 200 205  
 Leu Ala Ile Ser Gly Leu Arg Ser Glu Asp Glu Ala Asp Tyr Tyr Val  
 210 215 220  
 Ala Ala Trp Asp Asp Ser Leu Phe Val Phe Gly Gly Gly Thr Lys Leu  
 225 230 235 240  
 Thr Val Leu Gly Ala Ala  
 245

<210> 12  
 <211> 242  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Phage library

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 35 40 45  
 Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe  
 50 55 60  
 Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr  
 65 70 75 80  
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Arg Val Ala Pro Tyr Val Asn Thr Leu Val Phe Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly  
 115 120 125  
 Ser Gly Gly Ser Ala Leu Ser Ser Glu Leu Thr Gln Asp Pro Ala Val  
 130 135 140  
 Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys Gln Gly Asp Ser  
 145 150 155 160  
 Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala  
 165 170 175  
 Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro  
 180 185 190  
 Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile  
 195 200 205  
 Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg



210

215

220

Asp Ser Ser Gly Phe Thr Val Phe Gly Gly Gly Thr Lys Leu Thr Val  
 225 230 235 240

Leu Gly

<210> 13

<211> 240

<212> PRT

<213> Artificial Sequence

<220>

<223> Phage library

<400> 13

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 20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met  
 35 40 45

Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
 50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
 65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Arg Phe Ser Leu Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu  
 100 105 110

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly  
 115 120 125

Gly Ser Ala Leu Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser  
 130 135 140

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly  
 145 150 155 160

Ile Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro  
 165 170 175

Lys Leu Leu Val Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser  
 180 185 190

Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser  
 195 200 205

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Asn  
 210 215 220

Ser Tyr Arg Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg  
 225 230 235 240

<210> 14

<211> 742  
 <212> DNA  
 <213> Homo sapiens

<400> 14  
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 cctggccctg cactctcctg tttttcttc tcttcatccc tgtcttctgc aaagcaatgc 180  
 acgtggccca gcctgctgtg gtactggcca gcagccgagg catcgccagc tttgtgtgtg 240  
 agtatgcatc tccaggcaaa gccactgagg tccgggtgac agtgcttcgg caggctgaca 300  
 gccaggtgac tgaagtctgt gcggcaacct acatgatggg gaatgagttg accttcctag 360  
 atgattccat ctgcacgggc acctccagt gaaatcaagt gaacctcact atccaaggac 420  
 tgagggccat ggacacggga ctctacatct gcaagggtgga gctcatgtac ccaccgccat 480  
 actacctggg cataggcaac ggaacccaga tttatgtaat tgatccagaa ccgtgcccag 540  
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<210> 15  
 <211> 223  
 <212> PRT  
 <213> Homo sapiens

<400> 15  
 Met Ala Cys Leu Gly Phe Gln Arg His Lys Ala Gln Leu Asn Leu Ala  
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 Thr Arg Thr Trp Pro Cys Thr Leu Leu Phe Phe Leu Leu Phe Ile Pro  
 20 25 30  
 Val Phe Cys Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala  
 35 40 45  
 Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly  
 50 55 60  
 Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln  
 65 70 75 80  
 Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr  
 85 90 95  
 Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val  
 100 105 110  
 Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile  
 115 120 125  
 Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly  
 130 135 140  
 Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser  
 145 150 155 160  
 Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe  
 165 170 175  
 Tyr Ser Phe Leu Leu Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys  
 180 185 190  
 Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu  
 195 200 205

Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn  
 210 215 220

<210> 16  
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 <212> DNA  
 <213> Homo sapiens

<400> 16  
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 ctggatcgga cctggaacct gggcgagaca gtggagctga agtgccaggt gctgctgtcc 180  
 aacccgacgt cgggctgctc gtggctcttc cagccgcgcg gcgccgccgc cagtcccacc 240  
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 aggaaccgaa gacgtgtttg caaatgtccc cggcctgtgg tcaaactcggg agacaagccc 720  
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<210> 17  
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 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence: primer

<400> 17  
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<210> 18  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 18  
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<210> 19  
 <211> 60  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 19  
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<210> 20  
 <211> 25

<212> DNA  
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 <210> 21  
 <211> 22  
 <212> DNA  
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 <223> Description of Artificial Sequence: primer  
 <400> 21  
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 <210> 22  
 <211> 30  
 <212> DNA  
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 <223> Description of Artificial Sequence: primer  
 <400> 22  
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 <210> 23  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence  
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 <223> Description of Artificial Sequence: primer  
 <400> 23  
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 <210> 26  
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 <210> 27  
 <211> 73  
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 <210> 28  
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 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: linker  
  
 <400> 28  
 Gly Gly Ser Gly Gly Ala Ala  
 1 5  
  
 <210> 29  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: hexapeptide motif  
  
 <400> 29  
 Met Tyr Pro Pro Pro Tyr  
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 <210> 30  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence  
  
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<223> Description of Artificial Sequence: hexapeptide motif

<400> 30

Leu Tyr Pro Pro Pro Tyr  
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<210> 31

<211> 223

<212> PRT

<213> Homo sapiens

<400> 31

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Ala Arg Thr Trp Pro Cys Thr Leu Leu Phe Phe Leu Leu Phe Ile Pro  
20 25 30

Val Phe Cys Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala  
35 40 45

Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly  
50 55 60

Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln  
65 70 75 80

Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr  
85 90 95

Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val  
100 105 110

Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile  
115 120 125

Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly  
130 135 140

Asn Gly Ala Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser  
145 150 155 160

Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe  
165 170 175

Tyr Ser Phe Leu Leu Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys  
180 185 190

Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu  
195 200 205

Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn  
210 215 220

<210> 32

<211> 221

<212> PRT

<213> Bos taurus

<400> 32

Met Ala Cys Ser Gly Phe Gln Ser His Gly Thr Trp Trp Thr Ser Arg  
1 5 10 15

Thr Trp Pro Cys Thr Ala Leu Phe Phe Leu Val Phe Ile Pro Val Phe  
 20 25 30  
 Ser Lys Gly Met Asn Val Thr Gln Pro Pro Val Val Leu Ala Ser Ser  
 35 40 45  
 Arg Gly Val Ala Ser Phe Ser Cys Glu Tyr Glu Ser Ser Gly Lys Ala  
 50 55 60  
 Asp Glu Val Arg Val Thr Val Leu Arg Glu Ala Gly Ser Gln Val Thr  
 65 70 75 80  
 Glu Val Cys Ala Gly Thr Tyr Met Val Glu Asp Glu Leu Thr Phe Leu  
 85 90 95  
 Asp Asp Ser Thr Cys Ile Gly Thr Ser Arg Gly Asn Lys Val Asn Leu  
 100 105 110  
 Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Val Cys Lys  
 115 120 125  
 Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Val Gly Ile Gly Asn Gly  
 130 135 140  
 Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Phe  
 145 150 155 160  
 Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe Tyr Ser  
 165 170 175  
 Phe Leu Ile Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys Arg Ser  
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 Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu Pro Glu  
 195 200 205  
 Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn  
 210 215 220

<210> 33  
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 <212> DNA  
 <213> Homo sapiens

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 gccagcctg ctgtggtact ggccagcagc cgaggcatcg ccagctttgt gtgtgagtat 180  
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 gtgactgaag tctgtgcggc aacctacatg atggggaatg agttgacctt cctagatgat 300  
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 gccatggaca cgggactcta catctgcaag gtggagctca tgtaccacc gccatactac 420  
 ctgggcatag gcaacggagc ccagatttat gtaattgatc cagaaccgtg cccagattct 480  
 gacttctctc tctggatcct tgcagcagtt agttcggggg tgttttttta tagctttctc 540  
 ctcacagctg tttctttgag caaaatgcta aagaaaagaa gccctcttac aacaggggtc 600  
 tatgtgaaaa tgccccaac agagccagaa tgtgaaaagc aatttcagcc ttattttatt 660  
 cccatcaatt ga 672

<210> 34  
 <211> 666  
 <212> DNA

<213> Bos taurus

<400> 34

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cctccagtgg tgctggctag cagccggggt gttgccagct tctcatgtga atatgagtct 180
tcaggcaaag ctgacgaggt ccgggtgaca gtgctgcggg aggcaggcag ccaggtgacc 240
gaagtctgtg ctgggaccta catggtggag gatgagctaa ccttcctgga tgattccact 300
tgcatggca cctccagagg aaacaaagt aacctacca tccaagggt gagggccatg 360
gacactgggc tctatgtctg caaagtggag ctcatgtacc cgccgcccta ctacgtgggc 420
atcggcaatg gaaccagat ttacgtcatt gatccagaac catgcccgga ttctgatttt 480
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gctgtttctt tgagcaaaat gctaaagaaa agaagccctc ttactacagg ggtctatgtg 600
aaaatgcccc caacagagcc agaatgtgaa aagcaatttc agccttattt tattcccatc 660
aattga
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<210> 35

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: linker

<400> 35

Gly Gly ser Gly Gly  
1 5